

SEQUENCE LISTING

SEQ ID NO: 1:

GGCTCCTCATCTGGAACACCTCGGGTCACCCCCGACAACGGTGGTGGGAGGGAGAGCGGC	60
CTCCTCCTCCCTGGTGGGGCCTGTCTGGGTGAAGCCCCTCTGTTCCCGAGGATCGTCCCA	120
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TGGGTTTGCCCCAATGACCGGCAGCTTGCCCTTCGAGCCAAGCTGCAGACGGGCTGGTCC	240
GTGCACACCTACCAGACGGAGAAGCAGAGGAGGAAGCAGCACCTCAGCCCGGCGGAGGTG	300
GAGGCCATCCTGCAGGTCATCCAGAGGGCAGAGCGGCTCGACGTCCTGGAGCAGCAGAGA	360
ATCGGGCGGCTGGTGGAGCGGCTGGAGACCATGAGGCGGAATGTGATGGGGAACGGCCTG	420
TCCCAGTGTCTGCTCTGCGGGGAGGTGCTGGGCTTCCTGGGCAGCTCGTCGGTGTCTGC	480
AAAGACTGCAGGAAGGTCTGGAAGAGGTGCGGGGGCCTGGTTCTACAAAGGGCTCCCCAAG	540
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CGAGGAAGAGTGGTTTCCAGTGACAGTGACAGTGAAGTCTAGCTCCTCCAGCCTA	720
GAGGACAGACTCCCATCCACTGGGGTCAGGGACCGGAAAGGCGACAAACCCTGGAAGGAG	780
TCAGGTGGCAGCGTGGAGGCCCCCAGGATGGGGTTCACCCAACCCGCGGGCCACCTCTTT	840
GGGTGTCAGAGCAGCCTGGCCAGTGGTGAGACGGGCACAGGCTCTGCTGACCCGCCAGGG	900
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AGCTGCCTGGGCTGAGGTGTCTGGTGCCTGGAACAGACTTCCCTGTGGAGGATTCCTGCC	1080
AGACCCTGCCCCGGCTCCTCCCTGACCGGTCTTGTGCCCTCACCAGACACCCTGTTGGCC	1140
ATGACTCAACAAACCAGTGTTGGGAGCCGTCTGCCTCCCCAGCTCAGTGCCTTTCTGCAC	1200
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CGGTGGGGCTATCTCCGTTGCTATATTAATGGCAAGACTAAATGAAACCTAGGGCACGGC	1440
CTCCGAAGCTGCGTGTGGCCCCCTTAGAGGTGAGCATCAGAGCCAGAGCAGTGAGGGGGAG	1500
ACTACCCACCCTCTCCCTCTCCCTTCAGCTCTGGGAGGCAGGCGCAGTGCCCCCCTCCC	1560
ATGGGCTGGCCCAGGACCGCGGGTGAAACCTGGGTCTGTTTAGTTTCTTTGGTTTTTGTA	1620
TGTTTGTGTTTGTGTTTGTGACACAGTCTCGCTTTGTTGCCCAGGCTGGGGTGCAGTGGCACGA	1680
TCGCGGCTCACTGCAACCTCCACCTCCCGGGCTCAAGCGATTCTCTCACCTCAGCCTCCT	1740
GAGTAGGTGGGATTACAGATGCCCCGCCACCACACCCAGTTAATTTTTGTATTTTAGAAG	1800
AGATGGGGTTTCTCCATGTTGGCCAGGCTGGTCTTGAACCTCCTGGTCTCAAGTGATCCGC	1860
CCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACCGCACCCAATCCTATT	1920
AGGTTTCTTTGAATCCCCCTCATGGCCTGCCTGGTTTTTGCTCAGCCTGTCTTCAGCTTGA	1980

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GGAGCTGGGAAGCTCTGGTGGATGCTATGAACTCACTTGCTGAAGAGCAGCGTTCAGGTG 2040
CATCCCCAGCCAGGGCACGTGGCTCCCTCAGCCATGAATTCACCTTCTCTTCAGGAGGTTT 2100
GGCTTGGCATGAAAATACTTCATTGAGAGTATGGGCAAATGCTTCTGGAAAACCCTTCCC 2160
TGAAGAGAGAGAACGTGTGTGTGTGTGTGCGGTGATCACACCCTCCCATCCTTCCTGCCTC 2220
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GGGCCCCCACCATTCACTTTTTGTCCTTGCTGCTGGCAAACAGTAAAGAAACTCACTTTC 2340
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SEQ ID NO: 2:

MetAlaAspThrIlePheGlySerGlyAsnAspGlnTrpValCysProAsnAspArgGln 20
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GlnArgArgLysGlnHisLeuSerProAlaGluValGluAlaIleLeuGlnValIleGln 60
ArgAlaGluArgLeuAspValLeuGluGlnGlnArgIleGlyArgLeuValGluArgLeu 80
GluThrMetArgArgAsnValMetGlyAsnGlyLeuSerGlnCysLeuLeuCysGlyGlu 100
ValLeuGlyPheLeuGlySerSerSerValPheCysLysAspCysArgLysValTrpLys 120
ArgSerGlyAlaTrpPheTyrLysGlyLeuProLysTyrIleLeuProLeuLysThrPro 140
GlyArgAlaAspGluProGlnPheArgProTrpProThrGluProAlaGluArgGluPro 160
ArgSerSerGluThrSerArgIleTyrThrTrpAlaArgGlyArgValValSerSerAsp 180
SerAspSerAspSerAspLeuSerSerSerSerLeuGluAspArgLeuProSerThrGly 200
ValArgAspArgLysGlyAspLysProTrpLysGluSerGlyGlySerValGluAlaPro 220
ArgMetGlyPheThrGlnProAlaGlyHisLeuPheGlyLeuGlnSerSerLeuAlaSer 240
GlyGluThrGlyThrGlySerAlaAspProProGlyGlyGlyThrGlySerAlaAspPro 260
ProGlyGlyProArgProGlyLeuThrArgArgAlaProValLysAspThrProGlyArg 280
AlaProAlaAlaAspAlaAlaProAlaGlyProSerSerCysLeuGly 296

SEQ ID NO: 3:

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TGGGTTTGCCCCAATGACCGGCAGCTTGCCCTTCGAGCCAAGCTGCAGACGGGCTGGTCC 240
GTGCACACCTACCAGACGGAGAAGCAGAGGAGGAAGCAGCACCTCAGCCCGGCGGAGGTG 300
GAGGCCATCCTGCAGGTCATCCAGAGGGCAGAGCGGCTCGACGTCCTGGAGCAGCAGAGA 360
ATCGGGCGGCTGGTGGAGCGGCTGGAGACCATGAGGCGGAATGTGATGGGGAACGGCCTG 420
TCCCAGTGTCTGCTCTGCGGGGAGGTGCTGGGCTTCCTGGGCAGCTCGTCGGTGTCTGC 480

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CGGCCCCCTGTGGCTGTGTAAGATCTGCAGTGAGCAAAGAGAGGTCTGGAAGAGGTCTGGGG	600
GCCTGGTTCTACAAAGGGCTCCCCAAGTATATCTTGCCCCTGAAGACCCCTGGCCGAGCT	660
GATGACCCCCACTTCCGACCTTTGCCCACGGAACCGGCAGAGCGAGAGCCCAGAAGCTCT	720
GAGACCAGCCGCATCTACACGTGGGCCCCGAGGAAGAGTGGTTTCCAGTGACAGTGACAGT	780
GA CTCGGATCTTAGCTCCTCCAGCCTAGAGGACAGACTCCCATCCACTGGGGTCAGGGAC	840
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TTCA C CCAACCCGCGGGCCACCTCTTTGGGTTCAGAGCAGCCTGGCCAGTGGTGAGACG	960
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CCCCGCCCCGGGCTGACCCGAAGGGCCCCGGTAAAAGACACACCTGGACGAGCCCCCGCT	1080
GCTGACGCAGCTCCAGCAGGCCCTCCAGCTGCCTGGGCTGAGGTGTCTGGTGCTGGAA	1140
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GTGCCCTCACCAGACACCCTGTTGGCCATGACTCAACAAACCAGTGTGGGAGCCGTCTG	1260
CCTCCCCAGCTCAGTGCCTTTCTGCACCCCTTCTCTCCTGGGGAGCTGTCTGCATCCGCC	1320
ACCCCTCCAACCACTGCCCTCAGCCCCCGACCTTATTTATTACCCTCCCCTCCCACACC	1380
CCCAATCTACCTGGTGATGATTTTAAGTTTGCGCGTGTCTTGGGTGGGCTGGGGGGTTT	1440
CCCACATGCAGTGTGAGAGGGGCGCCCGGTGGGGCTATCTCCGTTGCTATATTAATGGC	1500
AAGACTAAATGAAACCTAGGGCACGGCCTCCGAAGCTGCGTGTGGCCCCCTTAGAGGTGAG	1560
CATCAGAGCCAGAGCAGTGAGGGGGGAGACTCACCCACCCTCTCCCTCTCCCTTCAGCTCT	1620
GGGAGGCAGGCGCAGTGCCCCCCTCCCATGGGCTGGCCCAGGACCGCGGGTGAAACCTGG	1680
GTCTGTTTAGTTTCTTTGGTTTTTTGTATGTTTGTTTGTTTTTGACACAGTCTCGCTTTGT	1740
TGCCCAGGCTGGGGTGCAGTGGCACGATCGCGGCTCACTGCAACCTCCACCTCCCGGGCT	1800
CAAGCGATTCTCTCACCTCAGCCTCCTGAGTAGGTGGGATTACAGATGCCCGCCACCACA	1860
CCCAGTTAATTTTTGTATTTTTAGAAAGAGATGGGGTTTCTCCATGTTGGCCAGGCTGGTC	1920
TTGAACTCCTGGTCTCAAGTGATCCGCCCCGCTCGGCCTCCCAAAGTGCTGGGATTACAG	1980
GTGTGAGCCACCGCACCCAATCCTATTAGGTTTCTTTGAATCCCCTCATGGCCTGCCTGG	2040
TTTTTGCTCAGCCTGTCTTCAGCTTGAGGAGCTGGGAAGCTCTGGTGGATGCTATGAACT	2100
CACTTGCTGAAGAGCAGCGTTCAGGTGCATCCCCAGCCAGGGCACGTGGCTCCCTCAGCC	2160
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GGCAAATGCTTCTGGAAAACCCTTCCCTGAAGAGAGAGAACGTGTGTGTGTGTGTCGGTG	2280
ATCACACCCTCCCATCCTTCCTGCCTCCTGCCCCAAACCCCGGGTTCCTGGGTCTGGAAG	2340
GGCCTTCTCTCCAAGCTGGGAGCTCCTGGGCCCCCACCATTCACTTTTTGTCCTTGCTGC	2400
TGGCAAACAGTAAAGAAACTCACTTTCCTGTGGCACGTTATGCTTCAGAATTAAACAA	2460
TGAAGATTAAAA	2472

SEQ ID NO: 4:

MetAlaAspThrIlePheGlySerGlyAsnAspGlnTrpValCysProAsnAspArgGln	20
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GlnArgArgLysGlnHisLeuSerProAlaGluValGluAlaIleLeuGlnValIleGln	60
ArgAlaGluArgLeuAspValLeuGluGlnGlnArgIleGlyArgLeuValGluArgLeu	80
GluThrMetArgArgAsnValMetGlyAsnGlyLeuSerGlnCysLeuLeuCysGlyGlu	100
ValLeuGlyPheLeuGlySerSerSerValPheCysLysAspCysArgLysLysValCys	120
ThrLysCysGlyIleGluAlaSerProGlyGlnLysArgProLeuTrpLeuCysLysIle	140
CysSerGluGlnArgGluValTrpLysArgSerGlyAlaTrpPheTyrLysGlyLeuPro	160
LysTyrIleLeuProLeuLysThrProGlyArgAlaAspAspProHisPheArgProLeu	180
ProThrGluProAlaGluArgGluProArgSerSerGluThrSerArgIleTyrThrTrp	200
AlaArgGlyArgValValSerSerAspSerAspSerAspSerAspLeuSerSerSerSer	220
LeuGluAspArgLeuProSerThrGlyValArgAspArgLysGlyAspLysProTrpLys	240
GluSerGlyGlySerValGluAlaProArgMetGlyPheThrGlnProAlaGlyHisLeu	260
PheGlyLeuGlnSerSerLeuAlaSerGlyGluThrGlyThrGlySerAlaAspProPro	280
GlyGlyGlyThrGlySerAlaAspProProGlyGlyProArgProGlyLeuThrArgArg	300
AlaProValLysAspThrProGlyArgAlaProAlaAlaAspAlaAlaProAlaGlyPro	320
SerSerCysLeuGly	325

SEQ ID NO: 5:

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TGGGTTTGCCCCAATGACCGGCAGCTTGCCCTTCGAGCCAAGCACTGACTGCACAGCAGT	240
GAACAGGACCAACACAGTCCCTGGTCTTAAAGCACAGGTGGGCAGAGGCTGCAGACGGGC	300
TGGTCGGTGCACACCTACCAGACGGAGAAGCAGAGGAGGAAGCAGCACCTCAGCCCGGCG	360
GAGGTGGAGGCCATCCTGCAGGTCATCCAGAGGGCAGAGCGGCTCGACGTCCTGGAGCAG	420
CAGAGAATCGGGCGGCTGGTGGAGCGGCTGGAGACCATGAGGCGGAATGTGATGGGGAAC	480
GGCCTGTCCCAGTGTCTGCTCTGCGGGGAGGTGCTGGGCTTCCTGGGCAGCTCGTCGGTG	540
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CAGAAGCGGCCCTGTGGCTGTGTAAGATCTGCAGTGAGCAAAGAGAGGTCTGGAAGAGG	660
TCGGGGGCTGGTTCTACAAAGGGCTCCCCAAGTATATCTTGCCCCTGAAGACCCCTGGC	720
CGAGCTGATGACCCCCACTTCCGACCTTTGCCCACGGAACCGGCAGAGCGAGAGCCCAGA	780
AGCTCTGAGACCAGCCGCATCTACACGTGGGCCCCGAGGAAGAGTGGTTTCCAGTGACAGT	840
GACAGTGACTCGGATCTTAGCTCCTCCAGCCTAGAGGACAGACTCCCATCCACTGGGGTC	900

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GGGGGACCCCGCCCCGGGCTGACCCGAAGGGCCCCGGTAAAAGACACACCTGGACGAGCC	1140
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CTGGAACAGACTTCCCTGTGGAGGATTCCCTGCCAGACCCTGCCCGGCTCCTCCCTGACCG	1260
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CGTCTGCCTCCCCAGCTCAGTGCCTTTCTGCACCCCTTCTCTCCTGGGGAGCTGTCTGCA	1380
TCCGCCACCCCTCCAACCACTGCCCTCAGCCCCCGACCTTATTTATTACCCTCCCCCTCC	1440
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AATGGCAAGACTAAATGAAACCTAGGGCACGGCCTCCGAAGCTGCGTGTGGCCCCTTAGA	1620
GGTGAGCATCAGAGCCAGAGCAGTGAGGGGGAGACTCACCCACCCTCTCCCTCTCCCTTC	1680
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ACCTGGGTCTGTTTAGTCTTCTTGGTTTTTGTATGTTTGTGTTTTTGACACAGTCTCG	1800
CTTTGTTGCCCAGGCTGGGGTGAGTGGCACGATCGCGGCTCACTGCAACCTCCACCTCC	1860
CGGGCTCAAGCGATTCTCTCACCTCAGCCTCCTGAGTAGGTGGGATTACAGATGCCCGCC	1920
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CTGGTCTTGAACCTCCTGGTCTCAAGTGATCCGCCCCGCTCGGCCTCCCAAAGTGCTGGGA	2040
TTACAGGTGTGAGCCACCGCACCCAATCCTATTAGGTTTCTTTGAATCCCCTCATGGCCT	2100
GCCTGGTTTTTTGCTCAGCCTGTCTTCAGCTTGAGGAGCTGGGAAGCTCTGGTGGATGCTA	2160
TGAACTCACTTGCTGAAGAGCAGCGTTCAGGTGCATCCCCAGCCAGGGCACGTGGCTCCC	2220
TCAGCCATGAATTCACCTTCTCTTCAGGAGGTTTGGCTTGGCATGAAAATACTTCATTCAG	2280
AGTATGGGCAAATGCTTCTGGAAAACCCTTCCCTGAAGAGAGAGAACGTGTGTGTGTGTG	2340
TCGGTGATCACACCCTCCCATCCTTCCTGCCTCCTGCCCCAAACCCCGGGTTCCTGGGTC	2400
TGGAAGGGCCTTCTCTCCAAGCTGGGAGCTCCTGGGCCCCCACCATTCACTTTTTGTCCT	2460
TGCTGCTGGCAAACAGTAAAGAACTCACTTTCCTGTGGCACGTTATGCTTCAGAATTA	2520
AAACAATGAAGATTAAAA	2538

SEQ ID NO: 6:

MetArgArgAsnValMetGlyAsnGlyLeuSerGlnCysLeuLeuCysGlyGluValLeu	20
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CysGlyIleGluAlaSerProGlyGlnLysArgProLeuTrpLeuCysLysIleCysSer	60
GluGlnArgGluValTrpLysArgSerGlyAlaTrpPheTyrLysGlyLeuProLysTyr	80
IleLeuProLeuLysThrProGlyArgAlaAspAspProHisPheArgProLeuProThr	100
GluProAlaGluArgGluProArgSerSerGluThrSerArgIleTyrThrTrpAlaArg	120

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GlyArgValValSerSerAspSerAspSerAspSerAspLeuSerSerSerSerLeuGlu	140
AspArgLeuProSerThrGlyValArgAspArgLysGlyAspLysProTrpLysGluSer	160
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ValLysAspThrProGlyArgAlaProAlaAlaAspAlaAlaProAlaGlyProSerSer	240
CysLeuGly	243

SEQ ID NO: 7:

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CCCCGCCCCGGGCTGACCCGAAGGGCCCCGGTAAAAGACACACCTGGACGAGCCCCCGCT	1200
GCTGACGCAGCTCCAGCAGGCCCCCTCCAGCTGCCTGGGCTGAGGTGTCTGGTGCCTGGAA	1260
CAGACTTCCTGTGGAGGATTCCTGCCAGACCCTGCCCGGCTCCTCCCTGACCGGTCCTT	1320
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ACCCCTCCAACCACTGCCCTCAGCCCCCGACCTTATTTATTACCCTCCCCTCCCACACC	1500
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CATCAGAGCCAGAGCAGTGAGGGGGAGACTCACCCACCCTCTCCCTCTCCCTTCAGCTCT	1740
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CAAGCGATTCTCTCACCTCAGCCTCCTGAGTAGGTGGGATTACAGATGCCCCGCCACCACA	1980
CCCAGTTAATTTTTGTATTTTTAGAAAGAGATGGGGTTTCTCCATGTTGGCCAGGCTGGTC	2040
TTGAACTCCTGGTCTCAAGTGATCCGCCCCGCTCGGCCTCCCAAAGTGCTGGGATTACAG	2100
GTGTGAGCCACCGCACCCAATCCTATTAGGTTTCTTTGAATCCCCTCATGGCCTGCCTGG	2160
TTTTTGCTCAGCCTGTCTTCAGCTTGAGGAGCTGGGAAGCTCTGGTGGATGCTATGAACT	2220
CACTTGCTGAAGAGCAGCGTTCAGGTGCATCCCCAGCCAGGGCACGTGGCTCCCTCAGCC	2280
ATGAATTCACCTTCTCTTCAGGAGGTTTGGCTTGGCATGAAAATACTTCATTCAGAGTATG	2340
GGCAAATGCTTCTGGAAAACCCTTCCCTGAAGAGAGAGAACGTGTGTGTGTGTGTCGGTG	2400
ATCACACCCTCCCATCCTTCCTGCCTCCTGCCCCAAACCCCGGGTTCCTGGGTCTGGAAG	2460
GGCCTTCTCTCCAAGCTGGGAGCTCCTGGGCCCCCACCATTCACTTTTTGTCCTTGCTGC	2520
TGGCAAACAGTAAAGAACTCACTTTCCCTGTGGCACGTTATGCTTCAGAATTAAACAA	2580
TGAAGATTAAAA	2592

SEQ ID NO: 8:

MetAlaAspThrIlePheGlySerGlyAsnAspGlnTrpValCysProAsnAspArgGln	20
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GlnArgArgLysGlnHisLeuSerProAlaGluValGluAlaIleLeuGlnValIleGln	60
ArgAlaGluArgLeuAspValLeuGluGlnGlnArgIleGlyArgLeuValGluArgLeu	80
GluThrMetArgArgAsnValMetGlyAsnGlyLeuSerGlnCysLeuLeuCysGlyGlu	100
ValLeuGlyPheLeuGlySerSerSerValPheCysLysAspCysArgLysLysValCys	120
ThrLysCysGlyIleGluAlaSerProGlyGlnLysArgProLeuTrpLeuCysLysIle	140
CysSerGluGlnArgGluValTrpLysArgSerGlyAlaTrpPheTyrLysGlyLeuPro	160
LysTyrIleLeuProLeuLysThrProGlyArgAlaAspAspProHisPheArgProLeu	180
ProThrGluProAlaGluArgGluProArgSerSerGluThrSerArgIleTyrThrTrp	200
AlaArgGlyArgValValGlyArgLysCys	210

SEQ ID NO: 9:

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CTCCTCCTCCCTGGTGGGGCCTGTCTGGGTGAAGCCCCTCTGTTCCCGAGGATCGTCCCA	120
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CAGAGAATCGGGCGGCTGGTGGAGCGGCTGGAGACCATGAGGCGGAATGTGATGGGGAAC	480
GGCCTGTCCCAGTGTCTGCTCTGCGGGGAGGTGCTGGGCTTCCTGGGCAGCTCGTCGGTG	540
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AGGGACCGGAAAGGCGACAAACCCTGGAAGGAGTCAGGTGGCAGCGTGGAGGCCCCCAGG	1080
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TCCGCCACCCCTCCAACCACTGCCCTCAGCCCCCGACCTTATTTATTACCCTCCCCTCC	1560
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AGCTCTGGGAGGCAGGCGCAGTGCCCCCTCCCATGGGCTGGCCAGGACCGCGGGTGAA	1860
ACCTGGGTCTGTTTAGTTTTCTTTGGTTTTTGTATGTTTGTGTTTTTGACACAGTCTCG	1920
CTTTGTTGCCAGGCTGGGGTGCAGTGGCACGATCGCGGCTCACTGCAACCTCCACCTCC	1980
CGGGCTCAAGCGATTCTCTCACCTCAGCCTCCTGAGTAGGTGGGATTACAGATGCCCGCC	2040
ACCACACCCAGTTAATTTTTGTATTTTTAGAAAGAGATGGGGTTTCTCCATGTTGGCCAGG	2100
CTGGTCTTGAACCTCTGGTCTCAAGTGATCCGCCCCGCTCGGCCTCCCAAAGTGCTGGGA	2160
TTACAGGTGTGAGCCACCGCACCCAATCCTATTAGGTTTTCTTTGAATCCCCTCATGGCCT	2220
GCCTGGTTTTTTGCTCAGCCTGTCTTCAGCTTGAGGAGCTGGGAAGCTCTGGTGGATGCTA	2280
TGAACTCACTTGCTGAAGAGCAGCGTTCAGGTGCATCCCCAGCCAGGGCACGTGGCTCCC	2340

TCAGCCATGAATTCACTTCTCTTCAGGAGGTTTGGCTTGGCATGAAAATACTTCATTCAG	2400
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TCGGTGATCACACCCTCCCATCCTTCCTGCCTCCTGCCCCAAACCCCGGGTTCCTGGGTC	2520
TGGAAGGGCCTTCTCTCCAAGCTGGGAGCTCCTGGGCCCCCACCATTCACTTTTTGTCCT	2580
TGCTGCTGGCAAACAGTAAAGAACTCACTTTCCTGTGGCACGTTATGCTTCAGAATTA	2640
AAACAATGAAGATTAAAA	2658

SEQ ID NO: 10:

MetArgArgAsnValMetGlyAsnGlyLeuSerGlnCysLeuLeuCysGlyGluValLeu	20
GlyPheLeuGlySerSerSerValPheCysLysAspCysArgLysLysValCysThrLys	40
CysGlyIleGluAlaSerProGlyGlnLysArgProLeuTrpLeuCysLysIleCysSer	60
GluGlnArgGluValTrpLysArgSerGlyAlaTrpPheTyrLysGlyLeuProLysTyr	80
IleLeuProLeuLysThrProGlyArgAlaAspAspProHisPheArgProLeuProThr	100
GluProAlaGluArgGluProArgSerSerGluThrSerArgIleTyrThrTrpAlaArg	120
GlyArgValValGlyArgLysCys	128

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